

to the involvement of NO also in this pathological state, in agreement with the high activity of iNOS found in neurons affected by AD [3]. Interestingly, as a common denominator, in both HaCmel+ and 7PA2 cells lactate levels increased with respect to controls, being this effect higher in the AD cells. The Warburg effect was evaluated in the presence of OXPHOS inhibitors showing that cells are able to compensate OXPHOS failure by a glycolytic burst; in the 7PA2 cells, however, the glycolytic increment appears insufficient to compensate for the energy failure as indicated by the overall ATP deficit.

doi:[10.1016/j.bbabbio.2014.05.006](https://doi.org/10.1016/j.bbabbio.2014.05.006)

S7.02

A common link for programmed cell death in humans and plants

Irene Diaz-Moreno, Jonathan Martinez-Fabregas, Katuska Gonzalez-Arzola, Antonio Diaz-Quintana, Miguel A. De la Rosa
Instituto de Bioquímica Vegetal y Fotosíntesis, cicCartuja, Universidad de Sevilla, Spain
CSIC, Spain
 E-mail address: idiamoreno@us.es

Programmed cell death (PCD) is a fundamental event for the development of multicellular organisms. In mammalian cells, early events in PCD involve the release of cytochrome c (Cc) from mitochondria to the cytoplasm to act at the first stages of the apoptotic process, playing a key role in assembling the apoptosome. In plants, PCD is part of a general process named hypersensitive response, where Cc is also released into the cytosol but its role in PCD remains veiled. Such highly conserved cytoplasmic location of Cc upon apoptotic stimuli lead to think of a common link for PCD in evolutionarily distant species, like humans and plants. To better understand the role of Cc in the onset of PCD in both humans and plants, a proteomic approach based on affinity chromatography with Cc as bait was used. Upon combining this approach and Bimolecular Fluorescence Complementation (BIFC), a total of 8 humans and 9 plants new proteins interacting with Cc under PCD were found [1,2]. These new PCD Cc-partners are involved in protein folding, translational regulation, oxidative stress, DNA damage, energetic and mRNA metabolism. Strikingly, some of the novel human Cc-targets are closely related to those for plant Cc, indicating that the evolutionarily well-conserved cytosolic Cc – appearing in organism from plant to mammals – interact with a wide range of targets on PCD. Modeling of the complexes between human and plant Cc with its counterparts shows how the heme crevice of Cc takes part of the complex interface in agreement with the vast majority of known redox adducts of Cc. However, in contrast to the high turnover rate of the mitochondrial Cc redox adducts, those occurring under PCD lead to the formation of rather stable nucleo-cytoplasmic ensembles, as inferred from Surface Plasmon Resonance (SPR) and Nuclear Magnetic Resonance (NMR) measurements. On the basis of these findings, we suggest that human and plant Cc interacts with pro-survival, anti-apoptotic proteins after its release into the cytoplasm. Then, Cc may interfere with cell survival pathways and unlock PCD in order to prevent the spatial and temporal co-existence of antagonist signals. This work has been sponsored by the Spanish Ministry of Economy and Competitiveness (BFU2012-31670) and the Regional Government of Andalusia (BIO198).

References

- [1] Martínez-Fábregas et al. (2013) Mol. Cell. Proteomics, 12, 3666–3676.
- [2] Martínez-Fábregas et al. Mol. Cell. Proteomics, <http://dx.doi.org/10.1074/mcp.M113.034322>.

doi:[10.1016/j.bbabbio.2014.05.007](https://doi.org/10.1016/j.bbabbio.2014.05.007)

S7.P1

The organization of the TOB/SAM complex of the slime mold *Dictyostelium discoideum* at the vegetative stage of its life cycle

Monika Antoniewicz^a, Olgierd Stobienia^a, Małgorzata Słocińska^b, Dorota Raczynska^c, Hanna Kmita^a, Małgorzata Wojtkowska^a

^aLaboratory of Bioenergetics, Institute of Molecular Biology and Biotechnology, Faculty of Biology, Adam Mickiewicz University, Poland

^bDepartment of Animal Physiology and Development, Institute of Experimental Biology, Faculty of Biology, Poland

^cLaboratory of Gene Expression, Institute of Molecular Biology and Biotechnology, Faculty of Biology, Poland

E-mail address: monika.a@amu.edu.pl

The TOB/SAM complex localized in the mitochondrial outer membrane assembles mitochondrial β -barrel proteins into the membrane. The group of β -barrel proteins includes crucial mitochondrial proteins for example Tom40 (forming channel within the TOM complex that is regarded as the gate into mitochondria for imported proteins) and VDAC (of fundamental significance for metabolite transport across the outer membrane of mitochondria). TOB/SAM complex is essential for the proper function of mitochondria and consequently for cell functioning. Interestingly, there are differences in the TOB/SAM complex subunit organization as have been shown for representatives of different phylogenetic lineages. The slime mold *Dictyostelium discoideum* is recognized as being of particular value as a research model for developmental biology and medicine. Importantly, life cycle of *D. discoideum* offers an unparalleled variety of phenotypes to study as different unicellular and multicellular stages and multiple cell types occur within the life cycle of the organism. Here we present our results concerning the TOB/SAM complex of unicellular form of *D. discoideum* (myxamoebae). The results of BN (blue native gel) and 2D SDS-PAGE suggest that molecular mass of the complex is about 250–350 kDa and the complex may be present in two forms. Experiments performed by black lipid membrane (BLM) technique indicate that the complex displays channel activity. Proteomic screening of *D. discoideum* mitochondrial outer membrane proteins by nanospray liquid chromatography tandem mass spectrometry (LC-MS/MS) allowed us identification of Tob55/Sam50 protein. The protein is an essential subunit of the complex of different organisms and belongs to β -barrel proteins able to form channels. Interestingly, using antibody against the protein N-terminus we observed its two forms in mitochondria. Accordingly, PCR products labeled with a fluorescent probe indicate the presence of two forms of the encoding gene. Results of bioinformatics analysis allowed us for identification of a putative second subunit of the complex that reveals sequence similarity with human metaxin. Further studies of the TOB/SAM complex subunit organization in cell representing different stages of *D. discoideum* life cycle are important to get the data concerning the involvement of the complex in processes decisive for a cell functional